APPLICATION NO.	FILING DATE	FIRST NAM
09/297,793	07/19/99	JOBLING

HM12/0823

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KUBE

ART UNIT	
1638	

DATE MAILED: 08/23/01

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks

Office Action Summary	Application No. 09/297,703	Applicant(s) JOBLING ET AL.	
	Examiner Anne Kubelik	Art Unit 1638	

-- *The MAILING DATE of this communication appears on the cover sheet with the correspondence address* --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE *3* MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *01 August 2001* .

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-11,16-27 and 32* is/are pending in the application.

4a) Of the above claim(s) *3,9 and 10* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1,2,4-8,11,16-27 and 32* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *19 July 1999* is/are: a)☐ accepted or b)☒ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

11)☐ The proposed drawing correction filed on _____ is: a)☐ approved b)☐ disapproved by the Examiner.

If approved, corrected drawings are required in reply to this Office action.

12)☐ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. §§ 119 and 120

13)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☒ All b)☐ Some * c)☐ None of:

1.☒ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____ .

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

14)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).

a) ☐ The translation of the foreign language provisional application has been received.

15)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☒ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449) Paper No(s) _____ .
4) ☐ Interview Summary (PTO-413) Paper No(s). _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: .

DETAILED ACTION

1. Applicant's election with traverse of Group I (claims 1-2, 4-8, 11, 16-27 and 32, drawn to nucleic acids encoding SEQ ID NO:29) in Paper No. 16 is acknowledged. The traversal is on the ground(s) that Cooke et al, the prior art cited by the examiner, discloses altering potato plants by using nucleic acids encoding starch branching enzyme (SBE) I, while the technical feature of instant application is drawn to altering cassava plants by using a portion of nucleic acids encoding SBE II. Thus, Applicant argues, Cooke et al has no bearing on the special technical feature of the instant application.

This is not found persuasive because claim 1 is directed to a nucleic acid encoding a polypeptide having any SBE activity and encoding a portion, of unspecified size, of SEQ ID NOs:29 or 31. As the nucleic acid taught by Cooke et al encodes a polypeptide having starch branching activity and shares at least one amino acid with SEQ ID NO:29 or 31, Cooke et al renders the technical feature nonspecial.

The requirement is still deemed proper and is therefore made FINAL.

Claims 3 and 9-10 are withdrawn from consideration, as being drawn to non-elected inventions.

Specification

2. A substitute specification excluding the claims is required pursuant to 37 CFR 1.125(a) for the following reasons:

An assigned sequence identifier must be used in all instances in the specification where a patent application discusses a sequence. See MPEP 2422.03. and 37 CFR 1.821(d).

The faint and irregular quality of the letters in the specification could result in printing errors.

A substitute specification filed under 37 CFR 1.125(a) must only contain subject matter from the original specification and any previously entered amendment under 37 CFR 1.121. If the substitute specification contains additional subject matter not of record, the substitute specification must be filed under 37 CFR 1.125(b) and must be accompanied by: 1) a statement that the substitute specification contains no new matter; and 2) a marked-up copy showing the amendments to be made via the substitute specification relative to the specification at the time the substitute specification is filed.

Drawings

3. The drawings are objected to for the reasons indicated on accompanying form PTO 948. Correction is required.

Claim Objections

4. Claims 1, 6, 16 and 26 are objected to because they include nonelected sequences. Appropriate correction is required.

5. Claims 1-2, 6, 16 and 26 are objected to because sequences are referred by figure number rather than SEQ ID NO:. An assigned sequence identifier must be used in all instances in the claims where a patent application discusses a sequence. See MPEP 2422.03. and 37 CFR 1.821(d).

Claim Rejections - 35 USC § 101

6. 35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

7. Claims 1-2, 4-8, 11 and 32 are rejected under 35 U.S.C. 101 because the claimed invention is directed to non-statutory subject matter. The claims are drawn to a nucleic acid sequence, which reads on a product of nature.

The DNA molecule, as claimed, has the same characteristics and utility as those found naturally in the genome or as cellular precursors thereof and therefore does not constitute patentable subject matter. See *American Wood v. Fiber Disintegrating Co.*, 90 U.S. 566 (1974), *American Fruit Growers v. Brogdex Co.*, 283 U.S. 2 (1931), *Funk Brothers Seed Co. v. Kalo Inoculant Co.*, 33 U.S. 127 (1948), *Diamond v. Chakrabarty*, 206 USPQ 193 (1980). It is suggested that the claims be modified to refer to the hand of the inventor, *e.g.* by replacing "A" with --An isolated-- or --A purified--.

8. Claims 1-2, 4-8, 11, 16-27 and 32 are rejected under 35 U.S.C. 101 because the claimed invention is not supported by either a specific asserted utility or a well established utility.

The claims are drawn to nucleic acids that have 200 base pair regions with 88% identity to SEQ ID NO:28 and that encode proteins with SBE activity. These nucleic acids include those that encode SBE I enzymes (*e.g.*, Burton et al, 1995, Plant J. 7:3-15; see below), but the instant specification only teaches the use of nucleic acids encoding SBE II enzymes, but not the use of nucleic acids encoding SBE I enzymes alone or with nucleic acids encoding other SBE I enzymes (as in claims 20-21). Thus, the instant application fails to teach a specific utility for nucleic acids encoding SBE I enzymes.

Claim Rejections - 35 USC § 112

9. The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

10. Claims 1, 4, 6-8, 11 and 16-27 are also rejected under 35 U.S.C. 112, first paragraph. Specifically, since the claimed invention is not supported by either a specific asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention.

11. Claims 1-2, 4-8, 11, 16-27 and 32 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for nucleic acids of SEQ ID NO:28 and nucleic acids encoding SEQ ID NO:29, certain methods of using those nucleic acids, and plants transformed with those nucleic acids, does not reasonably provide enablement for other methods of using those nucleic acids, nor for nucleic acids encoding portions of SEQ ID NO:29 or that hybridize to SEQ ID NO:28 under conditions of unspecified stringency or that have 200 base pair regions with 88% identity to SEQ ID NO:28, methods of using those nucleic acids, and plants transformed with those nucleic acids. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention commensurate in scope with these claims.

The claims are broadly drawn to nucleic acids that hybridize to SEQ ID NO:28, that encode some portion of SEQ ID NO:29, or that have 200 base pair regions with 88% identity to SEQ ID NO:28, methods of using those nucleic acids, and plants transformed with those nucleic acids

The instant specification, however, fails to provide guidance for which amino acids of SEQ ID NO:29 can be altered and to which other amino acids, and which amino acids must not be changed, to maintain SBE II activity of the encoded protein. The specification also fails to provide guidance for which amino acids can be deleted and which regions of the protein can tolerate insertions and still produce a functional enzyme.

It cannot be predicted by one of skill in the art that a nucleic acid that encodes only a portion of SEQ ID NO:29, that hybridizes to SEQ ID NO:28 under conditions of low or moderate stringency, or that has a 200 base pair region with 88% identity to SEQ ID NO:28 will encode a protein with SBE II activity. Bowie et al (1990, Science 247:1306-10) teach that an amino acid sequence encodes a message that determines the shape and function of a protein and that it is the ability of the protein to fold into unique three-dimensional structures that allows it to function and carry out the instructions of the genome. The cited reference also teaches that the prediction of protein structure from sequence data and, in turn, utilizing predicted structural determinations to ascertain functional aspects of the protein, is extremely complex (pg 1306, left column). Bowie et al teach that while it is known that many amino acid substitutions are possible in any given protein, the positions within the protein's sequence where such amino acid substitutions can be made with a reasonable expectation of maintaining function are limited. Certain positions in the sequence are critical to the three-dimensional structure/function relationship, and these regions can tolerate only conservative substitutions or none at all (pg 1306, right column).

The sensitivity of proteins to alterations in even a single amino acid in a sequence is exemplified by Lazar et al (1988, Mol. Cell. Biol. 8:1247-1252), who teach that a replacement of

aspartic acid at position 47 with alanine or asparagine in transforming growth factor alpha had no effect, but that replacement with serine or glutamic acid sharply reduced biological activity (see the abstract). Small changes in amino acid sequence can completely modify enzymatic function; Broun et al (1998, Science 282:1315-1317) teach that a change of four amino acids converts an oleate 12-desaturase to a hydroxylase. Thus, Lazar et al and Broun et al demonstrated that one or few amino acid substitutions could dramatically affect the biological activity and the structure-function characteristics of a protein.

Making "conservative" substitutions (*e.g.*, substituting one polar amino acid for another, or one acidic one for another) does not produce predictable results. Lazar et al (*supra*) showed that the "conservative" substitution of glutamic acid for aspartic acid at position 47 reduced biological function of transforming growth factor alpha while "nonconservative" substitutions with alanine or asparagine had no effect (abstract). Similarly, Hill et al (1998, Biochem. Biophys. Res. Comm. 244:573-577) teach when three histidines that are maintained in ADP-glucose pyrophosphorylase across several species are substituted with the "nonconservative" amino acid glutamine, there is little effect on enzyme activity, while the substitution of one of those histidines with the "conservative" amino acid arginine drastically reduced enzyme activity (see Table 1). All these mutated proteins, however, would have at least 95% identity to the original protein. The nucleic acids encoding all these mutated proteins, however, would hybridize under high stringency to the nucleic acids encoding the original protein.

Constructing an antisense RNA sequence that reliably inhibits gene expression is an unpredictable science. The effect of length of complementarity between the antisense construct and the target gene varies from gene to gene and organism to organism. It can not be predicted

which portion of a gene will work in antisense suppression of enzyme activity. An antisense RNA made to the 3' half of the chalcone synthase cDNA worked, while one made to the 5' half did not (van der Krol et al, 1990, Plant Mol. Biol. 14:457-466; see pg 459, right column, to pg 461, left column); however, in other systems, the 5' half of a gene has been effective (Bird et al, 1991, Bio/Technol. 9:635-639, see pg 636, left column, paragraph 1, and Table 1) and the 3' end has not worked (Kuipers et al, 1995, Mol. Gen. Genet. 246:745-755, see pg 747, right column, last paragraph).

Antisense constructs that are not completely homologous can have very unpredictable effects. Colliver et al (1997, Plant Mol. Biol. 35:509-522) showed that transformation of bird's foot trefoil with a construct that was antisense to bean chalcone synthase resulted in transformants with *increased* levels of chalcone synthase transcripts (pg 519, left column, paragraph 2) and note other instances when this phenomenon has occurred (pg 519, right column, paragraph 1).

Plants of different species in which the expression of the same gene is inhibited via antisense constructs can behave very differently. While tomatoes containing an antisense acid invertase DNA construct grew identically to control plants (Klann et al, 1996, Plant Physiol. 112:1321-1330; see the abstract and pg 1323, right column, paragraph 1), carrot development is drastically altered when acid invertase expression is reduced via an antisense construct (Tang et al, 1999, Plant Cell 11:177-189; see pg 179, left column, paragraphs 1-2, and pg 184, left column, paragraph 1).

Antisense inhibition of starch branching enzymes is unpredictable. Kossman et al (1995, Progress in Biotechnol., 10 (Carbohydrate Bioengineering): 271-278) teach that severe reduction

of the levels of the potato SBE RNA by antisense technology resulted in no change in chain length distribution or size of amylopectin in the tubers (pg 277, paragraph 9). Jobling et al (1999, Plant J. 18:163-171) teach that it is a minor form of SBE in tubers that is responsible for the amylopectin structure in potato (paragraph spanning pg 166-167 and paragraph 2 pg 167).

Thus, it can not be predicted that a nucleic acid encoding a "portion" of SEQ ID NO:29 or that a 200 bp or longer nucleic acid will inhibit the transcription or translation of the gene from which it was derived in the species from which it was derived, not can it be predicted that those nucleic acids will inhibit the transcription or translation of a homologous gene in another plant species.

Lastly, method of claims 20-21 uses at least a part of an SBE I gene; the size of that part is not specified. The instant specification fails to teach how a single nucleic acid, which constitutes part of an SBE I gene, can be used to interfere with the transcription or translation of the gene.

Given the claim breath, unpredictability, and lack of guidance as discussed above, undue experimentation would have been required by one skilled in the art to develop and evaluate nucleic acids that encode a multitude of portions of SEQ ID NO:29, that hybridize to SEQ ID NO:28 under conditions of unspecified stringency, or that have 200 base pair regions with 88% identity to SEQ ID NO:28, methods for their use, and plants transformed with them.

12. Claims 1-2, 4-8, 11, 16-27 and 32 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter that was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claims are broadly drawn to a multitude of DNA molecules that hybridize to SEQ ID NO:28 under conditions of unspecified stringency, that encode a multitude of "portions" of SEQ ID NO:29 of any length or sequence, or that have 200 base pair regions with 88% identity to SEQ ID NO:28. In contrast, the specification only describes a coding sequence from cassava that comprises SEQ ID NO:28 or that encodes SEQ ID NO:29.

The claims are not limited to nucleic acids that only encode SBE II enzymes, nor does the specification indicate if SEQ ID NO:29 is an SBE IIa or SBE IIb enzyme. Hence, Applicant has not, in fact, described all DNA molecules that encode an SBE, and the specification fails to provide an adequate written description of the claimed invention.

Therefore, given the lack of written description in the specification with regard to the structural and physical characteristics of the claimed compositions, and given the high level of unpredictability in this art, one skilled in the art would not have been in possession of the genus claimed at the time this application was filed.

See *University of California v. Eli Lilly*, 119 F.3d 1559, 43 USPQ 2d 1398 (Fed, Cir. 1997):

> The name cDNA is not in itself a written description of that DNA; it conveys no distinguishing information concerning its identity. While the example provides a process for obtaining human insulin-encoding cDNA, there is no further information in the patent pertaining to that cDNA's relevant structural or physical characteristics; in other words, it thus does not describe human insulin cDNA .... Accordingly, the specification does not provide a written description of the invention ....

See Amgen Inc. v. Chugai Pharmaceutical Co. Ltd., 18 USPQ 2d 1016 at page 1021:

> A gene is a chemical compound, albeit a complex one, and ... conception of a chemical compound requires that the inventor be able to define it so as to distinguish it from other materials .... Conception does not occur unless one has a mental picture of the structure of the chemical or is able to define it by its method of preparation, its physical or chemical properties, or whatever characteristics sufficiently distinguish it. It is not sufficient to define it solely by it principal biological property, *e.g.*, encoding human erythropoietin, because an alleged conception having no more specificity than that is simply a wish to know the identity of any material with that biological property.

13. The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

14. Claims 1-2, 4-8, 11, 16-27 and 32 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter that Applicant regards as the invention.

Dependent claims are included in all rejections.

Claim 1 is indefinite for its recitation of "an effective portion." The phrase "an effective portion" is not defined by the claim, the specification does not provide a standard for ascertaining the requisite degree, and one of ordinary skill in the art would not be reasonably apprised of the metes and bounds of the invention. The number of amino acids that comprise this portion is not clear, nor it is clear for what the portion is effective.

Claims 6, 16 and 26 are indefinite for their recitation of "the corresponding region". It is not clear what nucleotides are encompassed by this region, nor is the size of this region clear.

Claim 2 is indefinite for its recitation of "functionally equivalent nucleotide sequence". It is not clear is this sequence encodes the same protein as that of SEQ ID NO:29, if it encodes a protein with the same enzymatic activity as that of SEQ ID NO:29, or if it simply encodes a protein. For purposes of examination, the latter two were assumed. Such treatment does not relieve Applicant of the responsibility to respond to this rejection.

Claim 5 is indefinite for its recitation of "having the amino acid sequence NSKH at about residue 697." First, it is indefinite in its recitation of the abbreviation "NSKH." For purposes of examination, it was assumed that "NSKH" referred to "Asn-Ser-Lys-His." Such treatment does not relieve Applicant of the responsibility to respond to this rejection. Second, the location of the sequence is not clear; it is not clear which residues are included in those at "about" 697.

The phrase "stringent hybridization conditions" in claim 2 is a relative phrase that renders the claims indefinite. The phrase "stringent hybridization conditions" is not defined by the claims, the specification does not provide a standard for ascertaining the requisite degree, and one of ordinary skill in the art would not be reasonably apprised of the metes and bounds of the invention. As the stringency is not claimed or defined, all possible hybridization stringencies were assumed for purposes of examination.

Claim 21 recites the limitation "the cassava SBE I gene" in line 2. There is insufficient antecedent basis for this limitation in the claim.

Claims 20-21 are indefinite for their recitation of "at least a part of". How many nucleotides are part of this nucleic acid sequence is not clear. For purposes of examination, it was assumed that one nucleotide comprises at least a part of an SBE I gene. Such treatment does not relieve Applicant of the responsibility to respond to this rejection.

Claim 22 is not written in proper Markush format. The claims should be in the format "**selected from the group consisting of** A, B, C **and** D." "one of the following:" should be replaced with --the group consisting of-- and "or" should be replaced with --and--. See MPEP 2173.05(h). Additionally, each plant should be referred to as plant cells (*i.e.*, replace "cassava" with --cassava cell--, *etc.*).

In claim 23 it is unclear which starch properties differ from those of starch from an unaltered cell.

Claims 24-25 are indefinite in their recitation of "growing" as plants are --regenerated-- from plant cells.

Claims 16 recites the limitation "said transcript and/or translation product" in lines 5-6 and claim 18 recites the limitation "said transcripts and/or translation products" in line 4. There is insufficient antecedent basis for these limitations in the claims.

Claims 16 and 18 are indefinite in their recitation of "homologous gene". It is not clear to what the gene is homologous, nor is it clear which gene is being referred to.

Claim 27 is indefinite for being drawn to a plant according to claim 24, as claim 24 is drawn to a method. Additionally, the dependence of the claim on claim 24 as well as claims 16-22 makes it very unclear as to how the plant was produced. It is suggested that claim 24 be amended to be dependent upon any one of claims 16-22, and that claim 27 be amended to recite --A plant produced by the method of claim 24.--

15. Claims 16-24 are rejected under 35 U.S.C. 112, second paragraph, as being incomplete for omitting essential steps, such omission amounting to a gap between the steps. See MPEP § 2172.01. Method steps must be circular; the final step must generate the item the method is intended to produce. For example, the method of altering a plant cell in claim 16 ends in the causing the transcription of a nucleic acid into a cell, when it should end in the production of an altered plant cell.

Claim Rejections - 35 USC § 102

16. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

17. Claims 1-2, 4, 6-8, 11 and 32 are rejected under 35 U.S.C. 102(b) as being anticipated by Burton et al (1995, GenBank Accession No. X80009 and Plant J. 7:3-15).

Burton et al teach a pea nucleic acid that has a 200 base pair region (nucleotides 2052-2255) with 88% identity to SEQ ID NO:28 and that encodes a protein with SBE I activity (see sequence search results). As this 200 bp region has 88% identity to SEQ ID NO:28, the nucleic acid meets the criteria of claim 6, and because it is at least 300 bp long, it meets those of claim 7. This nucleic acid would hybridize to that of SEQ ID NO:28 under low stringency conditions and would be in a replicable nucleic acid construct with 5' and 3' untranslated regions for purposes of molecular biological manipulation. This nucleic acid would be operably linked to a plant promoter in the plant.

18. Claims 1-2, 4 and 11 are rejected under 35 U.S.C. 102(b) as being anticipated by Fisher et al (1996, GenBank Accession No. U22428 and Plant Mol. Biol. 30:97-108).

Fisher et al teach a nucleic acid that encodes an SBE II. This protein would share at least one amino acid with SEQ ID NO:29, and the nucleic acid would hybridize to SEQ ID NO:28 because it has 79% identity with it (see sequence search results). This nucleic acid would be in a replicable nucleic acid construct with 5' and 3' untranslated regions for purposes of molecular biological manipulation.

Claim Rejections - 35 USC § 103

19. The following is a quotation of 35 U.S.C. 103(a), which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person

having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

20. Claims 1-2, 4, 6-8, 11, 16-17, 22-27 and 32 are rejected under 35 U.S.C. 103(a) as being unpatentable over Hofvander et al (WO 92/11375) in view of each of Burton et al (*supra*) and Fisher et al (*supra*).

The claims are drawn to nucleic acids encoding an SBE, methods of using those nucleic acids to alter a plant host cell, plants produced by those methods, and a method of obtaining starch from those plants.

Hofvander et al disclose a method of using antisense constructs of nucleic acids encoding an SBE to alter a plant host cell, plants produced by those methods, and a method of obtaining starch from those plants (pg 6-11). Hofvander et al do not disclose the use of nucleic acids encoding other SBE enzymes.

Burton et al teach a pea nucleic acid that has a 200 base pair region (nucleotides 2052-2255) with 88% identity to SEQ ID NO:28 and that encodes a protein with SBE I activity, as discussed above.

Fisher et al teach a nucleic acid that encodes an SBE II. This protein would share at least one amino acid with SEQ ID NO:29, and the nucleic acid would hybridize to SEQ ID NO:28 because it has 79% identity with it, as discussed above.

At the time the invention was made, it would have been obvious to one of ordinary skill in the art to alter a plant hosts cell by antisense inhibition of an SBE enzyme as taught by Hofvander et al, and to modify that to use the nucleic acids encoding SBE described in each of Burton et al and Fisher et al. One of ordinary skill in the art would have been motivated to do so

because suppression of SBE genes in other economically important plant species would produce other altered starches.

21. Claims 18-21 are free of the prior art, given the failure of the prior art to teach or suggest methods of suppressing in a plant both the SBEII and SBEI genes or of suppressing SBE I by transformation with two SBE I genes. Claim 5 is free of the prior art, given the failure of the prior art to teach or suggest an isolated nucleic acid that encodes a polypeptide with SBE activity, that encodes a portion of SEQ ID NO:28, and that has the amino acid sequence Asn-Ser-Lys-His at about residue 697. Additionally, isolated nucleic acids encoding SEQ ID NO:29 are free of the prior art.

Conclusion

22. No claim is allowed.

23. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Anne R. Kubelik, whose telephone number is (703) 308-5059. The examiner can normally be reached on Monday through Friday, 8:15 am - 4:45 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Paula Hutzell, can be reached on (703) 308-4310. The fax phone numbers for the organization where this application or proceeding is assigned are (703) 308-4242 for regular communications and (703) 308-4242 for After Final communications.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is (703) 308-0196.

Anne R. Kubelik, Ph.D.
August 20, 2001

DAVID T. FOX
PRIMARY EXAMINER
GROUP ~~180~~ 1638